



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/966,264B  
Source: OIPF  
Date Processed by STIC: 9/26/02

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
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<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
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4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202



Does Not Comply  
Corrected Diskette Needed

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/966,264B

DATE: 09/26/2002  
TIME: 16:35:57

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF4\09262002\I966264B.raw

3 <110> APPLICANT: Barber, Elizabeth K  
5 <120> TITLE OF INVENTION: Gene Expression Control Element DNA  
7 <130> FILE REFERENCE: 896034605001  
W--> 8 <140> CURRENT APPLICATION NUMBER: US 09/966,264B  
C--> 9 <141> CURRENT FILING DATE: 2002-09-16  
11 <150> PRIOR APPLICATION NUMBER: US 60/237,079  
12 <151> PRIOR FILING DATE: 2000-09-30  
14 <160> NUMBER OF SEQ ID NOS: 61  
16 <170> SOFTWARE: PatentIn version 3.1

#### ERRORED SEQUENCES

772 <210> SEQ ID NO: 51  
773 <211> LENGTH: 1236  
774 <212> TYPE: DNA  
775 <213> ORGANISM: human  
777 <400> SEQUENCE: 51

E--> 779 tag ttt cct att caa tgt ata gtg cac caa agg tca att caa gag (-192)  
780 Phe Pro Ile Gln Cys Ile Val His Gln Arg Ser Ile Gln Glu  
781 -75 -70 -65

E--> 783 ttt att att att att ttc aac cca agt aaa agc aga gag aaa ata gcc (-144)  
784 Phe Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala  
785 -60 -55 -50

E--> 787 acc tcc acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg (-96)  
788 Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu  
789 -45 -40 -35

E--> 791 aaa tga aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc (-48)  
792 Lys Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr  
793 -30 -25 -20

E--> 795 tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg gat ggt (0) → no 0!  
796 Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met Asp Gly  
797 -15 -10 -5

E--> 799 gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag 48  
800 Val Val Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu  
801 1 5 10 15

E--> 803 taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96  
804 Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro  
805 20 25 30

E--> 807 atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga 144  
808 Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly  
809 35 40 45

E--> 811 att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat 192

→ cannot have negative numbers  
- must count as a total  
and continuous  
e.g. -end no. should  
be 45, 93, and  
soon.  
See § 1.822(c)(6)  
of the rules.

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```

      812 Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala His
      813          50          55          60
E--> 815 ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta 240
      816 Phe Ser Met Thr Pro Val Ala Ser Asn Ile Lys Leu Ile Leu
      817          65          70          75
E--> 819 aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg 288
      820 Thr Asn Asn Val Trp Leu His Gly Phe Ala Ser Ser Trp
      821          80          85
E--> 823 aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt 336
      824 Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu
      825          90          95          100
E--> 827 ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa 384
      828 Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys
      829 105          110          115          120
E--> 831 gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt 432
      832 Glu Thr Glu Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe
      833          125          130          135
E--> 835 ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg 480
      836 Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met
      837          140          145          150
E--> 839 gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca 528
      840 Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr
      841          155          160          165
E--> 843 gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat 576
      844 Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His
      845          170          175          180
E--> 847 ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt 624
      848 Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe
      849          185          190          195
E--> 851 aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt 672
      852 Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys
      853          200          205          210
E--> 855 aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag 720
      856 Arg Phe Gln Phe Leu Ser Leu Leu Leu Phe Cys Gln Trp Gln
      857          215          220          225
E--> 859 gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca 768
      860 Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr
      861          230          235          240
E--> 863 tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816
      864 Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr
      865          245          250          255
E--> 867 cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864
      868 His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr
      869          260          265          270
E--> 871 aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912
      872 Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr
      873          275          280
E--> 875 cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
      876 Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg

```

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```

      877 285                290                295
E--> 879 aat agc atg aga agc cgt gtt tga tgt taa tta att          996
      880 Asn Ser Met Arg Ser Arg Val      Cys      Leu Ile
E--> 881 300                305
      969 <210> SEQ ID NO: 55
      970 <211> LENGTH: 1236
      971 <212> TYPE: DNA
      972 <213> ORGANISM: human
      974 <400> SEQUENCE: 55
      976 ctagtttcct attcaatgta tagtgcacca aaggtcaatt caagagttta    50
      978 ttattattat ttccaaccca agtaaaagca gagagaaaat agccacctcc    100
      980 accatagcct cagaagcaag ccaacagcct gaaacagctt tgaaatgaaa    150
      982 agttggtgtg gcggtgatgg tggcagtgat aatggtgacc gatggttggg    200
E--> 984 tgctggtgat ggtagtggtg gttgtga.ag gttggtgatgg tggtttgatt    250
      986 gatagtaaaa aaaatgttcg ttaatacaag tagagagtaa gtaatcaatc    300
      988 aatcactcat agccaagggtg gaaaagatgt atcccatcat ggaatattcc    350
      990 tgttctgata gaaatcttgt gcttatctat ggaattcttt tgatatatat    400
      992 ttacattggg aacctgaatg tagcttgaca tttttccatg taaacaccag    450
      994 tagcctgata caacattaag ctgatactaa caaacaacgt gtaatggctt    500
      996 cattaataag gctttgcttc ttcttgaaa ctggtgaaaa atcaaacctt    550
      998 gttgtgtaca ccctcgatgc agcttctgtg ttgtcttcac ccagaaatgg    600
      1000 ggaatgattt cccaaatggc aaagaaacag agtgatgcta tctatctgca    650
      1002 ccttttgtaa agtctgtctt tctttctctt tgttttccag gacacaatgt    700
      1004 aggaagtctt ttccacatgg cagatgattt gggcagagcg atggagtcct    750
      1006 tagtatcagt catgacagat gaagaaggag cagaataaat gttttacaac    800
      1008 tcctgattcc cgcattggtt ttataatatt eatacaacaa agaggattag    850
E--> 1010 acagtaagag tttacaagaa at.aaatcta tatttttgtg aagggtagtg    900
      1012 gtattatact gtagatttca gtagtttcta agtctgttat tgttttgtaa    950
      1014 acaatggcag gttttacacg tctatgcaat tgtacaaaaa agttataaga   1000
      1016 aaactacatg taaaatcttg atagctaaat aacttgccat ttctttatat   1050
      1018 ggaacgcatt ttgggttggt taaaaattta taacagttat aaagaaagaa   1100
      1020 ttataaagga aaaagaaaat aacgcaatgg acaagtgggtg aagctgtgaa   1150
      1022 ctgaggtgtg cacaattatc aggaacaccc caaaaccaa gtgaggtaga   1200
      1024 aatagcatga gaagccgtgt ttgatgttaa ttaatt                    1236

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delete

## VERIFICATION SUMMARY

DATE: 09/26/2002

PATENT APPLICATION: US/09/966,264B

TIME: 16:35:58

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09262002\I966264B.raw

L:8 M:283 W: Missing Blank Line separator, <140> field identifier  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:779 M:254 E: No. of Bases conflict, LENGTH:Input:-192 Counted:46 SEQ:51  
M:254 Repeated in SeqNo=51  
L:881 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1236 Found:1237 SEQ:51  
L:984 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:1010 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:1116 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=58